



SEQUENCE LISTING

<110> Daniel Cohen
Ilya Chumakov

<120> Treatment of CNS Disorders Using D-Amino Acid Oxidase and D-Aspartate
Oxidase Antagonists

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<150> 60/261,883

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 gtttggtact tccggctgct gca atg cgt gtg gtg gtg att gga gca gga gtc 173
 Met Arg Val Val Val Ile Gly Ala Gly Val
 1 5 10
 atc ggg ctg tcc acc gcc ctc tgc atc cat gag cgc tac cac tca gtc 221
 Ile Gly Leu Ser Thr Ala Leu Cys Ile His Glu Arg Tyr His Ser Val
 15 20 25
 ctg cag cca ctg gac ata aag gtc tac gcg gac cgc ttc acc cca ctc 269
 Leu Gln Pro Leu Asp Ile Lys Val Tyr Ala Asp Arg Phe Thr Pro Leu
 30 35 40
 acc acc acc gac gtg gct gcc ggc ctc tgg cag ccc tac ctt tct gac 317
 Thr Thr Thr Asp Val Ala Ala Gly Leu Trp Gln Pro Tyr Leu Ser Asp
 45 50 55
 ccc aac aac cca cag gag gcg acc ctt cct gga agg aca cag ttc tgg 365
 Pro Asn Asn Pro Gln Glu Ala Thr Leu Pro Gly Arg Thr Gln Phe Trp
 60 65 70
 gat ttc gga agc tgacccccag agagctggat atgttcccag attacggcta 417
 Asp Phe Gly Ser
 75
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 aagggttaact gagagggggag tgaagttctt ccagcggaaa gtggagtctt ttgaggaggt 537
 ggcaagagaa ggcgcagacg tgattgtcaa ctgcactggg gtatgggctg gggcgctaca 597
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Met
1
cgt gtg gtg gtg att gga gca gga gtc atc ggg ctg tcc acc gcc ctg 164
Arg Val Val Val Ile Gly Ala Gly Val Ile Gly Leu Ser Thr Ala Leu
5 10 15
tgc atc cat gag cgc tac cac tca gtc ctg cag cca ctg gac ata aag 212
Cys Ile His Glu Arg Tyr His Ser Val Leu Gln Pro Leu Asp Ile Lys
20 25 30
gtc tac gcg gac cgc ttc acc cca ctg acc acc acc gac gtg gct gcc 260
Val Tyr Ala Asp Arg Phe Thr Pro Leu Thr Thr Thr Asp Val Ala Ala
35 40 45
ggc ctg tgg cag ccc tac ctt tct gac ccc aac aac cca cag gag gcg 308
Gly Leu Trp Gln Pro Tyr Leu Ser Asp Pro Asn Asn Pro Gln Glu Ala
50 55 60 65
gac tgg agc caa cag acc ttt gac tat ctg agc cat gtc cat tct 356
Asp Trp Ser Gln Gln Thr Phe Asp Tyr Leu Leu Ser His Val His Ser
70 75 80
ccc aac gct gaa aac ctg ggc ctg ttc cta atc tcg ggc tac aac ctg 404
Pro Asn Ala Glu Asn Leu Gly Leu Phe Leu Ile Ser Gly Tyr Asn Leu
85 90 95
ttc cat gaa gcc att ccg gtg gca aga gaa ggc gca gac gtg att gtc 452
Phe His Glu Ala Ile Pro Val Ala Arg Glu Gly Ala Asp Val Ile Val
100 105 110
aac tgc act ggg gta tgg gct ggg gcg cta caa cga gac ccc ctg ctg 500
Asn Cys Thr Gly Val Trp Ala Gly Ala Leu Gln Arg Asp Pro Leu Leu
115 120 125
cag cca ggc cgg ggg cag atc atg aag gtg gac gcc cct tgg atg aag 548
Gln Pro Gly Arg Gly Gln Ile Met Lys Val Asp Ala Pro Trp Met Lys
130 135 140 145
cac ttc att ctg acc cat gac cca gag aga ggc atc tac aat tcc ccg 596

His	Phe	Ile	Leu	Thr	His	Asp	Pro	Glu	Arg	Gly	Ile	Tyr	Asn	Ser	Pro		
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Tyr	Ile	Ile	Pro	Gly	Thr	Gln	Thr	Val	Thr	Leu	Gly	Gly	Ile	Phe	Gln		
			165					170					175				
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Leu	Gly	Asn	Trp	Ser	Glu	Leu	Asn	Asn	Ile	Gln	Asp	His	Asn	Thr	Ile		
		180					185				190						
tgg	gaa	ggc	tgc	tgc	aga	ctg	gag	ccc	aca	ctg	aag	aat	gca	aga	att	740	
Trp	Glu	Gly	Cys	Cys	Arg	Leu	Glu	Pro	Thr	Leu	Lys	Asn	Ala	Arg	Ile		
	195					200				205							
att	ggt	gaa	cga	act	ggc	ttc	cgg	cca	gta	cgc	ccc	cag	att	cgg	cta	788	
Ile	Gly	Glu	Arg	Thr	Gly	Phe	Arg	Pro	Val	Arg	Pro	Gln	Ile	Arg	Leu		
210					215				220					225			
gaa	aga	gaa	cag	ctt	cgc	act	gga	cct	tca	aac	aca	gag	gtc	atc	cac	836	
Glu	Arg	Glu	Gln	Leu	Arg	Thr	Gly	Pro	Ser	Asn	Thr	Glu	Val	Ile	His		
			230					235				240					
aac	tat	ggc	cat	gga	ggc	tac	ggg	ctc	acc	atc	cac	tgg	gga	tgt	gcc	884	
Asn	Tyr	Gly	His	Gly	Gly	Tyr	Gly	Leu	Thr	Ile	His	Trp	Gly	Cys	Ala		
		245					250				255						
ctg	gag	gca	gcc	aag	ctc	ttt	ggg	aga	atc	ctg	gaa	gaa	aag	aaa	ttg	932	
Leu	Glu	Ala	Ala	Lys	Leu	Phe	Gly	Arg	Ile	Leu	Glu	Glu	Lys	Lys	Leu		
	260					265				270							
tcc	aga	atg	cca	cca	tcc	cac	ctc	tgaagactcc	agtgactgct	gcctcccccc						986	
Ser	Arg	Met	Pro	Pro	Ser	His	Leu										
	275				280												
acaagaactc	ccttctcccc	tcagccaatg	aatcaatgtg	ctccttcata	agccattgct	1046											
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<211> 347

<212> PRT

<213> Homo sapiens

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			20					25				30					
Lys	Val	Tyr	Ala	Asp	Arg	Phe	Thr	Pro	Leu	Thr	Thr	Thr	Asp	Val	Ala		
		35				40					45						
Ala	Gly	Leu	Trp	Gln	Pro	Tyr	Leu	Ser	Asp	Pro	Asn	Asn	Pro	Gln	Glu		
	50				55				60								
Ala	Asp	Trp	Ser	Gln	Gln	Thr	Phe	Asp	Tyr	Leu	Leu	Ser	His	Val	His		
65				70					75					80			
Ser	Pro	Asn	Ala	Glu	Asn	Leu	Gly	Leu	Phe	Leu	Ile	Ser	Gly	Tyr	Asn		
		85						90				95					
Leu	Phe	His	Glu	Ala	Ile	Pro	Asp	Pro	Ser	Trp	Lys	Asp	Thr	Val	Leu		
		100						105				110					
Gly	Phe	Arg	Lys	Leu	Thr	Pro	Arg	Glu	Leu	Asp	Met	Phe	Pro	Asp	Tyr		
		115				120					125						
Gly	Tyr	Gly	Trp	Phe	His	Thr	Ser	Leu	Ile	Leu	Glu	Gly	Lys	Asn	Tyr		

130		135		140
Leu Gln Trp Leu Thr Glu Arg Leu Thr Glu Arg Gly Val Lys Phe Phe				
145		150		155
Gln Arg Lys Val Glu Ser Phe Glu Glu Val Ala Arg Glu Gly Ala Asp				
	165		170	175
Val Ile Val Asn Cys Thr Gly Val Trp Ala Gly Ala Leu Gln Arg Asp				
	180		185	190
Pro Leu Leu Gln Pro Gly Arg Gly Gln Ile Met Lys Val Asp Ala Pro				
	195		200	205
Trp Met Lys His Phe Ile Leu Thr His Asp Pro Glu Arg Gly Ile Tyr				
	210		215	220
Asn Ser Pro Tyr Ile Ile Pro Gly Thr Gln Thr Val Thr Leu Gly Gly				
225		230		235
Ile Phe Gln Leu Gly Asn Trp Ser Glu Leu Asn Asn Ile Gln Asp His				
	245		250	255
Asn Thr Ile Trp Glu Gly Cys Cys Arg Leu Glu Pro Thr Leu Lys Asn				
	260		265	270
Ala Arg Ile Ile Gly Glu Arg Thr Gly Phe Arg Pro Val Arg Pro Gln				
	275		280	285
Ile Arg Leu Glu Arg Glu Gln Leu Arg Thr Gly Pro Ser Asn Thr Glu				
	290		295	300
Val Ile His Asn Tyr Gly His Gly Gly Tyr Gly Leu Thr Ile His Trp				
305		310		315
Gly Cys Ala Leu Glu Ala Ala Lys Leu Phe Gly Arg Ile Leu Glu Glu				
	325		330	335
Lys Lys Leu Ser Arg Met Pro Pro Ser His Leu				
	340		345	

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<212> PRT

<213> Homo sapiens

<400> 8

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	20
Lys Val Tyr Ala Asp Arg Phe Thr Pro Leu Thr Thr Thr Asp Val Ala	25
	35
Ala Gly Leu Trp Gln Pro Tyr Leu Ser Asp Pro Asn Asn Pro Gln Glu	40
	50
Ala Asp Trp Ser Gln Gln Thr Phe Asp Tyr Leu Leu Ser His Val His	55
65	70
Ser Pro Asn Ala Glu Asn Leu Gly Leu Phe Leu Ile Ser Gly Tyr Asn	60
	85
Leu Phe His Glu Ala Ile Pro Asp Pro Ser Trp Lys Asp Thr Val Leu	90
	100
Gly Phe Arg Lys Leu Thr Pro Arg Glu Leu Asp Met Phe Pro Asp Tyr	105
	115
Gly Tyr Gly Trp Phe His Thr Ser Leu Ile Leu Glu Gly Lys Asn Tyr	120
	130
Leu Gln Trp Leu Thr Glu Arg Leu Thr Glu Arg Gly Val Lys Phe Phe	135
145	150
Gln Arg Lys Val Glu Ser Phe Glu Glu Val Ala Arg Glu Gly Ala Asp	155
	165
Val Ile Val Asn Cys Thr Gly Val Trp Ala Gly Ala Leu Gln Arg Asp	170
	175

		180					185				190				
Pro	Leu	Leu	Gln	Pro	Gly	Arg	Gly	Gln	Ile	Met	Lys	Asp	Pro	Asp	Ser
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Tyr	Ser	Trp	Arg	His	Leu	Pro	Val	Gly	Lys	Leu	Glu				
		210				215					220				

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			20					25					30		
Lys	Val	Tyr	Ala	Asp	Arg	Phe	Thr	Pro	Leu	Thr	Thr	Thr	Asp	Val	Ala
		35				40					45				
Ala	Gly	Leu	Trp	Gln	Pro	Tyr	Leu	Ser	Asp	Pro	Asn	Asn	Pro	Gln	Glu
	50					55					60				
Ala	Thr	Leu	Pro	Gly	Arg	Thr	Gln	Phe	Trp	Asp	Phe	Gly	Ser		
65					70				75						

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 <213> Homo sapiens

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Leu	Cys	Ile	His	Glu	Arg	Tyr	His	Ser	Val	Leu	Gln	Pro	Leu	Asp	Ile
			20					25					30		
Lys	Val	Tyr	Ala	Asp	Arg	Phe	Thr	Pro	Leu	Thr	Thr	Thr	Asp	Val	Ala
		35				40					45				
Ala	Gly	Leu	Trp	Gln	Pro	Tyr	Leu	Ser	Asp	Pro	Asn	Asn	Pro	Gln	Glu
	50					55					60				
Ala	Asp	Trp	Ser	Gln	Gln	Thr	Phe	Asp	Tyr	Leu	Leu	Ser	His	Val	His
65					70				75						80
Ser	Pro	Asn	Ala	Glu	Asn	Leu	Gly	Leu	Phe	Leu	Ile	Ser	Gly	Tyr	Asn
			85					90					95		
Leu	Phe	His	Glu	Ala	Ile	Pro	Val	Ala	Arg	Glu	Gly	Ala	Asp	Val	Ile
		100						105					110		
Val	Asn	Cys	Thr	Gly	Val	Trp	Ala	Gly	Ala	Leu	Gln	Arg	Asp	Pro	Leu
		115					120					125			
Leu	Gln	Pro	Gly	Arg	Gly	Gln	Ile	Met	Lys	Val	Asp	Ala	Pro	Trp	Met
		130				135					140				
Lys	His	Phe	Ile	Leu	Thr	His	Asp	Pro	Glu	Arg	Gly	Ile	Tyr	Asn	Ser
145					150				155					160	
Pro	Tyr	Ile	Ile	Pro	Gly	Thr	Gln	Thr	Val	Thr	Leu	Gly	Gly	Ile	Phe
			165					170					175		
Gln	Leu	Gly	Asn	Trp	Ser	Glu	Leu	Asn	Ile	Gln	Asp	His	Asn	Thr	
		180						185				190			
Ile	Trp	Glu	Gly	Cys	Cys	Arg	Leu	Glu	Pro	Thr	Leu	Lys	Asn	Ala	Arg
		195					200					205			
Ile	Ile	Gly	Glu	Arg	Thr	Gly	Phe	Arg	Pro	Val	Arg	Pro	Gln	Ile	Arg
		210				215					220				


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Leu Glu Arg Glu Gln Leu Arg Thr Gly Pro Ser Asn Thr Glu Val Ile
225                230                235                240
His Asn Tyr Gly His Gly Gly Tyr Gly Leu Thr Ile His Trp Gly Cys
                245                250                255
Ala Leu Glu Ala Ala Lys Leu Phe Gly Arg Ile Leu Glu Glu Lys Lys
                260                265                270
Leu Ser Arg Met Pro Pro Ser His Leu
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attaaaatag cttgtaggat tactcatttt crtttttctt ctttttaa ataaagcaat      180
gtcatcactt ttttccctgt attatatctt tcctcaataa ttgatatgct acattaaagg      240
aacacaaaat ggtcttaatt atgcaataat gatcaaggca aagagtgttt cctgggaact      300
aatgggttgcc tgagaggagg tgatggcttg aggtccagct gggtattaag ccgcaggaaa      360
tgctgcaggc caagatttgt attatttctc tgagatgaaa atgaacccaa aaaaaggcaa      420
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<210> 12
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<213> Homo sapiens

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<223> 99-5919-215 : polymorphic base A or G

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<222> 203..227

<223> 99-5919-215.probe

<220>

<221> primer_bind

<222> 196..214

<223> 99-5919-215.mis

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<221> primer_bind

<222> 216..234

<223> 99-5919-215.mis complement

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<222> 11..29

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<221> primer_bind

<222> 445..465

<223> 99-5919.rp complement

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actcacagaa	atcacctttt	cctgtataca	tttttaggat	gtcagacttt	attctaata	180
tttctcctag	ttgcccccca	aaattgtatt	ctacrgtgtg	attttaaagc	tgaattttca	240
agatgatatt	tcatatctat	attttcacaa	gcttttcttc	tatgaatggt	attgtcagct	300
gtcaggggtg	gagatggtac	ttgatactac	attctttcca	agctggtgcc	tgaatcggtt	360
taagacaaag	tcattactag	gctgtaaact	gttgctctgc	aaaattgagc	agcacgtatt	420
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<212> DNA

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<222> 509..742

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<221> polyA_signal

<222> 718..723

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<222> 21

<223> 8-135-112 : polymorphic base C or T

<220>

<221> allele

<222> 75

<223> 8-135-166 : polymorphic base A or C

<220>

<221> allele

<222> 135

<223> 99-16038-118 : polymorphic base A or G

<220>

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<222> 194

<223> 8-137-152 : polymorphic base G or T

<220>

<221> allele

<222> 224

<223> 8-137-182 : polymorphic base A or G

<220>

<221> allele

<222> 390

<223> 8-130-220 : polymorphic base A or C

<220>

<221> allele

<222> 406

<223> 8-130-236 : polymorphic base A or G

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<221> allele

<222> 578

<223> 8-131-199 : polymorphic base A or C

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<222> 641

<223> 8-132-97 : polymorphic base C or T

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<221> allele

<222> 708

<223> 8-132-164 : polymorphic base C or T

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<221> allele
 <222> 723
 <223> 8-132-179 : polymorphic base A or T

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 <222> 135
 <223> Xaa=Lys or Arg

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 Lys Leu Met Gly Ala Asp Xaa Leu Gln Leu Phe Arg Ser Arg Tyr Thr
 5 10 15
 ttg ggt aaa atc tac ttc ata ggt ttt caa arg agc att ctt ctg agc 151
 Leu Gly Lys Ile Tyr Phe Ile Gly Phe Gln Xaa Ser Ile Leu Leu Ser
 20 25 30 35
 aaa tct gaa aac tct cta aac tct att gca aag gag aca gaa kaa gga 199
 Lys Ser Glu Asn Ser Leu Asn Ser Ile Ala Lys Glu Thr Glu Xaa Gly
 40 45 50
 aga gag acg gta aca agg aaa gaa rga tgg aag aga agg cat gag gac 247
 Arg Glu Thr Val Thr Arg Lys Glu Xaa Trp Lys Arg Arg His Glu Asp
 55 60 65
 ggc tat ttg gaa atg gca cag agg cat tta cag aga tca tta tgt cct 295
 Gly Tyr Leu Glu Met Ala Gln Arg His Leu Gln Arg Ser Leu Cys Pro
 70 75 80
 tgg gtc tct tac ctt cct cag ccc tat gca gag ctt gaa gaa gta agc 343
 Trp Val Ser Tyr Leu Pro Gln Pro Tyr Ala Glu Leu Glu Glu Val Ser
 85 90 95
 agc cat gtt gga aaa gtc ttc atg gca aga aac tat gag ttc ctt gmc 391
 Ser His Val Gly Lys Val Phe Met Ala Arg Asn Tyr Glu Phe Leu Xaa
 100 105 110 115
 tat gag gcc tct aar gac cgc agg cag cct cta gaa cga atg tgg acc 439
 Tyr Glu Ala Ser Lys Asp Arg Arg Gln Pro Leu Glu Arg Met Trp Thr
 120 125 130

tgc aac tac aac cag caa aaa gac cag tca tgc aac cac aag gaa ata	487
Cys Asn Tyr Asn Gln Gln Lys Asp Gln Ser Cys Asn His Lys Glu Ile	
135 140 145	
act tct acc aaa gct gaa tgagtttgga agcagattct tcccagccaa	535
Thr Ser Thr Lys Ala Glu	
150	
tcttctgat gacaatgtag tctggccaac atcttcaactg gamtctgacg gactctgtgt	595
ctgggaccca gctgataaca cgtgggtgatg ggattgtatt tgcaaytctc tggtcagtaa	655
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ttattaawtg tgcttcaagt tttaaca	742

<210> 14
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 <213> Homo sapiens

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<220>
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220

4213 PEPTIDE

<222> 124..153

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[illegible]

<210> 15

<211> 476

<212> DNA

<213> Homo sapiens

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1				5					10				15					
tta	tgt	cct	tgg	gtc	tct	tac	ctt	cct	cag	ccc	tat	gca	gag	ctt	gaa		96	
Leu	Cys	Pro	Trp	Val	Ser	Tyr	Leu	Pro	Gln	Pro	Tyr	Ala	Glu	Leu	Glu			
			20					25				30						
gaa	gta	agc	agc	cat	gtt	gga	aaa	gtc	ttc	atg	gca	aga	aac	tat	gag		144	
Glu	Val	Ser	Ser	His	Val	Gly	Lys	Val	Phe	Met	Ala	Arg	Asn	Tyr	Glu			
		35					40					45						
ttc	ctt	gcc	tat	gag	gcc	tct	aag	gac	cgc	agg	cag	cct	cta	gaa	cga		192	
Phe	Leu	Ala	Tyr	Glu	Ala	Ser	Lys	Asp	Arg	Arg	Gln	Pro	Leu	Glu	Arg			
		50				55				60								
atg	tgg	acc	tgc	aac	tac	aac	cag	caa	aaa	gac	cag	tca	tgc	aac	cac		240	
Met	Trp	Thr	Cys	Asn	Tyr	Asn	Gln	Gln	Lys	Asp	Gln	Ser	Cys	Asn	His			
65				70					75				80					
aag	gaa	ata	act	tct	acc	aaa	gct	gaa	tgag	ttt	gga	agc	agatt	tct			287	
Lys	Glu	Ile	Thr	Ser	Thr	Lys	Ala	Glu										
			85															
tcc	cag	cca	tc	ttt	ctg	at	gaca	atg	tag	tct	ggc	caac	at	ctt	ca	ctg	gactctgacg	347

gactctgtgt ctgggaccca gctgataaca cgtggtgatg ggattgtatt tgcaactctc 407
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 atctctctt 476

<210> 16
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 <212> PRT
 <213> Homo sapiens

<400> 16
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 20 25 30
 Glu Val Ser Ser His Val Gly Lys Val Phe Met Ala Arg Asn Tyr Glu
 35 40 45
 Phe Leu Ala Tyr Glu Ala Ser Lys Asp Arg Arg Gln Pro Leu Glu Arg
 50 55 60
 Met Trp Thr Cys Asn Tyr Asn Gln Gln Lys Asp Gln Ser Cys Asn His
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 Lys Glu Ile Thr Ser Thr Lys Ala Glu
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<210> 17
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 <212> DNA
 <213> Homo sapiens

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 cccctcagga aatagcatcc tgtgtccccg cactgcagtt gtctgggtctc tccagcagtt 180
 tggtaacttcc ggctgctgca atg cgt gtg gtg gtg att gga gca gga gtc atc 233
 Met Arg Val Val Val Ile Gly Ala Gly Val Ile
 1 5 10
 ggg ctg tcc acc gcc ctc tgc atc cat gag cgc tac cac tca gtc ctg 281
 Gly Leu Ser Thr Ala Leu Cys Ile His Glu Arg Tyr His Ser Val Leu
 15 20 25
 cag cca ctg cac ata aag gtc tac gcg gac cgc ttc acc cca ctc acc 329
 Gln Pro Leu His Ile Lys Val Tyr Ala Asp Arg Phe Thr Pro Leu Thr
 30 35 40
 acc acc gac gtg gct gcc ggc ctc tgg cag ccc tac ctt tct gac ccc 377
 Thr Thr Asp Val Ala Ala Gly Leu Trp Gln Pro Tyr Leu Ser Asp Pro
 45 50 55
 aac aac cca cag gag gcg gac tgg agc caa cag acc ttt gac tat ctc 425
 Asn Asn Pro Gln Glu Ala Asp Trp Ser Gln Gln Thr Phe Asp Tyr Leu
 60 65 70 75
 ctg agc cat gtc cat tct ccc aac gct gaa aac ctg ggc ctg ttc cta 473
 Leu Ser His Val His Ser Pro Asn Ala Glu Asn Leu Gly Leu Phe Leu
 80 85 90
 atc tcg ggc tac aac ctc ttc cat gaa gcc att ccg gac cct tcc tgg 521
 Ile Ser Gly Tyr Asn Leu Phe His Glu Ala Ile Pro Asp Pro Ser Trp
 95 100 105
 aag gac aca gtt ctg gga ttt cgg aag ctg acc ccc aga gag ctg gat 569
 Lys Asp Thr Val Leu Gly Phe Arg Lys Leu Thr Pro Arg Glu Leu Asp
 110 115 120
 atg ttc cca gat tac ggc tat ggc tgg ttc cac aca agc cta att ctg 617

Met	Phe	Pro	Asp	Tyr	Gly	Tyr	Gly	Trp	Phe	His	Thr	Ser	Leu	Ile	Leu	
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gag	gga	aag	aac	tat	cta	cag	tgg	ctg	act	gaa	agg	tta	act	gag	agg	665
Glu	Gly	Lys	Asn	Tyr	Leu	Gln	Trp	Leu	Thr	Glu	Arg	Leu	Thr	Glu	Arg	
140					145				150					155		
gga	gtg	aag	ttc	ttc	cag	cgg	aaa	gtg	gag	tct	ttt	gag	gag	gtg	gca	713
Gly	Val	Lys	Phe	Phe	Gln	Arg	Lys	Val	Glu	Ser	Phe	Glu	Glu	Val	Ala	
			160						165					170		
aga	gaa	ggc	gca	gac	gtg	att	gtc	aac	tgc	act	ggg	gta	tgg	gct	ggg	761
Arg	Glu	Gly	Ala	Asp	Val	Ile	Val	Asn	Cys	Thr	Gly	Val	Trp	Ala	Gly	
			175					180					185			
ggg	cta	caa	cga	gac	ccc	ctg	ctg	cag	cca	ggc	cgg	ggg	cag	atc	atg	809
Ala	Leu	Gln	Arg	Asp	Pro	Leu	Leu	Gln	Pro	Gly	Arg	Gly	Gln	Ile	Met	
		190				195					200					
aag	gtg	gac	gcc	cct	tgg	atg	aag	cac	ttc	att	ctc	acc	cat	gac	cca	857
Lys	Val	Asp	Ala	Pro	Trp	Met	Lys	His	Phe	Ile	Leu	Thr	His	Asp	Pro	
	205				210						215					
gag	aga	ggc	atc	tac	aat	tcc	ccg	tac	atc	atc	cca	ggg	acc	cag	aca	905
Glu	Arg	Gly	Ile	Tyr	Asn	Ser	Pro	Tyr	Ile	Ile	Pro	Gly	Thr	Gln	Thr	
220					225				230					235		
gtt	act	ctt	gga	ggc	atc	ttc	cag	ttg	gga	aac	tgg	agt	gaa	cta	aac	953
Val	Thr	Leu	Gly	Gly	Ile	Phe	Gln	Leu	Gly	Asn	Trp	Ser	Glu	Leu	Asn	
			240					245					250			
aat	atc	cag	gac	cac	aac	acc	att	tgg	gaa	ggc	tgc	tgc	aga	ctg	gag	1001
Asn	Ile	Gln	Asp	His	Asn	Thr	Ile	Trp	Glu	Gly	Cys	Cys	Arg	Leu	Glu	
		255						260					265			
ccc	aca	ctg	aag	aat	gca	aga	att	att	ggg	gaa	gca	act	ggc	ttc	cgg	1049
Pro	Thr	Leu	Lys	Asn	Ala	Arg	Ile	Ile	Gly	Glu	Ala	Thr	Gly	Phe	Arg	
		270				275						280				
cca	gta	cgc	ccc	cag	att	cgg	cta	gaa	aga	gaa	cag	ctt	cgc	act	gga	1097
Pro	Val	Arg	Pro	Gln	Ile	Arg	Leu	Glu	Arg	Glu	Gln	Leu	Arg	Thr	Gly	
	285					290				295						
cct	tca	aac	aca	gag	gtc	atc	cac	aac	tat	ggc	cat	gga	ggc	tac	ggg	1145
Pro	Ser	Asn	Thr	Glu	Val	Ile	His	Asn	Tyr	Gly	His	Gly	Gly	Tyr	Gly	
300					305				310					315		
ctc	acc	atc	cac	tgg	gga	tgt	gcc	ctg	gag	gca	gcc	aag	ctc	ttt	ggg	1193
Leu	Thr	Ile	His	Trp	Gly	Cys	Ala	Leu	Glu	Ala	Ala	Lys	Leu	Phe	Gly	
			320					325					330			
aga	atc	ctg	gaa	gaa	aag	aaa	ttg	tcc	aga	atg	cca	cca	tcc	cac	ctc	1241
Arg	Ile	Leu	Glu	Glu	Lys	Lys	Leu	Ser	Arg	Met	Pro	Pro	Ser	His	Leu	
		335					340					345				
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aatcaatgtg	ctccttcata	agccattgct	tctccctcac	ttctttctctc	aaagaagcat											1361
gaggtgagag	aaagccacra	agtcagtgcc	tggagaaggg	ttcagcccaa	catggggccc											1421
ctctcatcac	tgaaatccct	ctaccttctc	tgggtctggc	attataaaga	acagctgagg											1481
ctgtcattcc	atgagtcttc	agaagaaagg	acagctcaga	aagtcaaaga	ggccaactgc											1541
ccagagccac	agaaaatgga	ggataattga	ggctaagtaa	cctgattaca	agttgtacta											1601
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<210> 18

<211> 347

<212> PRT

<213> Homo sapiens

<400> 18

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Lys	Val	Tyr	Ala	Asp	Arg	Phe
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Ala	Gly	Leu	Trp	Gln	Pro	Tyr
		50		55		60
Ala	Asp	Trp	Ser	Gln	Gln	Thr
		65		70		75
Ser	Pro	Asn	Ala	Glu	Asn	Leu
		85		90		95
Leu	Phe	His	Glu	Ala	Ile	Pro
		100		105		110
Gly	Phe	Arg	Lys	Leu	Thr	Pro
		115		120		125
Gly	Tyr	Gly	Trp	Phe	His	Thr
		130		135		140
Leu	Gln	Trp	Leu	Thr	Glu	Arg
		145		150		155
Gln	Arg	Lys	Val	Glu	Ser	Phe
		165		170		175
Val	Ile	Val	Asn	Cys	Thr	Gly
		180		185		190
Pro	Leu	Leu	Gln	Pro	Gly	Arg
		195		200		205
Trp	Met	Lys	His	Phe	Ile	Leu
		210		215		220
Asn	Ser	Pro	Tyr	Ile	Ile	Pro
		225		230		235
Ile	Phe	Gln	Leu	Gly	Asn	Trp
		245		250		255
Asn	Thr	Ile	Trp	Glu	Gly	Cys
		260		265		270
Ala	Arg	Ile	Ile	Gly	Glu	Ala
		275		280		285
Ile	Arg	Leu	Glu	Arg	Glu	Gln
		290		295		300
Val	Ile	His	Asn	Tyr	Gly	His
		305		310		315
Gly	Cys	Ala	Leu	Glu	Ala	Ala
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Lys	Lys	Leu	Ser	Arg	Met	Pro
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<210> 19

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 19

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Ser	Thr	Ala	Val	Cys	Ile	Ser	Lys	Leu	Val	Pro	Arg	Cys	Ser	Val	Thr	
		20					25					30				
atc	att	tca	gac	aag	ttt	act	cca	gat	acc	acc	agt	gat	gtg	gca	gcc	144

Ile	Ile	Ser	Asp	Lys	Phe	Thr	Pro	Asp	Thr	Thr	Ser	Asp	Val	Ala	Ala	
		35					40					45				
gga	atg	ctt	att	cct	cac	act	tat	cca	gat	aca	ccc	att	cac	acg	cag	192
Gly	Met	Leu	Ile	Pro	His	Thr	Tyr	Pro	Asp	Thr	Pro	Ile	His	Thr	Gln	
	50					55					60					
aag	cag	tgg	ttc	aga	gaa	acc	ttt	aat	cac	ctc	ttt	gca	att	gcc	aat	240
Lys	Gln	Trp	Phe	Arg	Glu	Thr	Phe	Asn	His	Leu	Phe	Ala	Ile	Ala	Asn	
65				70						75					80	
tct	gca	gaa	gct	gga	gat	gct	ggg	gtt	cat	ttg	gta	tca	ggg	tgg	cag	288
Ser	Ala	Glu	Ala	Gly	Asp	Ala	Gly	Val	His	Leu	Val	Ser	Gly	Trp	Gln	
				85					90					95		
ata	ttt	cag	agc	act	ccg	act	gaa	gaa	gtg	cca	ttc	tgg	gct	gac	gtg	336
Ile	Phe	Gln	Ser	Thr	Pro	Thr	Glu	Glu	Val	Pro	Phe	Trp	Ala	Asp	Val	
		100						105					110			
gtt	ctg	gga	ttt	cga	aag	atg	act	gag	gct	gag	ctg	aag	aaa	ttc	ccc	384
Val	Leu	Gly	Phe	Arg	Lys	Met	Thr	Glu	Ala	Glu	Leu	Lys	Lys	Phe	Pro	
		115					120					125				
cag	tat	gtg	ttt	ggg	cag	gct	ttt	aca	acc	ctg	aaa	tgt	gaa	tgc	cct	432
Gln	Tyr	Val	Phe	Gly	Gln	Ala	Phe	Thr	Thr	Leu	Lys	Cys	Glu	Cys	Pro	
	130				135						140					
gcc	tac	ctc	ccg	tgg	ttg	gag	aaa	agg	ata	aag	gga	agt	gga	ggc	tgg	480
Ala	Tyr	Leu	Pro	Trp	Leu	Glu	Lys	Arg	Ile	Lys	Gly	Ser	Gly	Gly	Trp	
145				150						155					160	
aca	ctc	act	cgg	cga	ata	gaa	gac	ctg	tgg	gaa	ctt	cat	ccg	tcc	ttt	528
Thr	Leu	Thr	Arg	Arg	Ile	Glu	Asp	Leu	Trp	Glu	Leu	His	Pro	Ser	Phe	
				165					170					175		
gac	atc	gtg	gtc	aac	tgt	tca	ggc	ctt	gga	agc	aga	cag	ctt	gca	gga	576
Asp	Ile	Val	Val	Asn	Cys	Ser	Gly	Leu	Gly	Ser	Arg	Gln	Leu	Ala	Gly	
		180						185					190			
gac	tca	aag	att	ttc	cct	gta	agg	ggc	caa	gtc	ctc	caa	gtt	cag	gct	624
Asp	Ser	Lys	Ile	Phe	Pro	Val	Arg	Gly	Gln	Val	Leu	Gln	Val	Gln	Ala	
		195					200					205				
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Pro	Trp	Val	Glu	His	Phe	Ile	Arg	Asp	Gly	Ser	Gly	Leu	Thr	Tyr	Ile	
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Tyr	Pro	Gly	Thr	Ser	His	Val	Thr	Leu	Gly	Gly	Thr	Arg	Gln	Lys	Gly	
225				230						235					240	
gac	tgg	aat	ctg	tcc	ccg	gat	gca	gaa	aat	agc	aga	gag	att	ctt	tcc	768
Asp	Trp	Asn	Leu	Ser	Pro	Asp	Ala	Glu	Asn	Ser	Arg	Glu	Ile	Leu	Ser	
				245					250					255		
cga	tgc	tgt	gct	ctg	gag	ccc	tcc	ctc	cac	gga	gcc	tgc	aac	atc	agg	816
Arg	Cys	Cys	Ala	Leu	Glu	Pro	Ser	Leu	His	Gly	Ala	Cys	Asn	Ile	Arg	
			260					265					270			
gag	aag	gtg	ggc	ttg	agg	ccc	tac	agg	cca	ggc	gtg	cga	ctg	cag	aca	864
Glu	Lys	Val	Gly	Leu	Arg	Pro	Tyr	Arg	Pro	Gly	Val	Arg	Leu	Gln	Thr	
		275					280					285				
gag	ctc	ctt	gcg	cga	gat	gga	cag	agg	ctg	cct	gta	gtc	cac	cac	tat	912
Glu	Leu	Leu	Ala	Arg	Asp	Gly	Gln	Arg	Leu	Pro	Val	Val	His	His	Tyr	
		290				295					300					
ggc	cat	ggg	agt	ggg	ggc	atc	tca	gtg	cac	tgg	ggc	act	gct	ctg	gag	960
Gly	His	Gly	Ser	Gly	Gly	Ile	Ser	Val	His	Trp	Gly	Thr	Ala	Leu	Glu	
305				310						315					320	
gcc	gcc	agg	ctg	gtg	agc	gag	tgt	gtc	cat	gcc	ctc	agg	acc	ccc	att	1008
Ala	Ala	Arg	Leu	Val	Ser	Glu	Cys	Val	His	Ala	Leu	Arg	Thr	Pro	Ile	
				325					330					335		
ccc	aag	tca	aac	ctg	tagatgacat	aaaatgacag	caaagagact	gagagactgt								1063

Pro Lys Ser Asn Leu

340

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<210> 20

<211> 1023

<212> DNA

<213> Homo sapiens

<400> 20

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 Ser Thr Ala Val Cys Ile Ser Lys Leu Val Pro Arg Cys Ser Val Thr
 20 25 30
 atc att tca gac aag ttt act cca gat acc acc agt gat gtg gca gcc 144
 Ile Ile Ser Asp Lys Phe Thr Pro Asp Thr Thr Ser Asp Val Ala Ala
 35 40 45
 gga atg ctt att cct cac act tat cca gat aca ccc att cac acg cag 192
 Gly Met Leu Ile Pro His Thr Tyr Pro Asp Thr Pro Ile His Thr Gln
 50 55 60
 aag cag tgg ttc aga gaa acc ttt aat cac ctc ttt gca att gcc aat 240
 Lys Gln Trp Phe Arg Glu Thr Phe Asn His Leu Phe Ala Ile Ala Asn
 65 70 75 80
 tct gca gaa gct gga gat gct ggt gtt cat ttg gta tca ggg ata aag 288
 Ser Ala Glu Ala Gly Asp Ala Gly Val His Leu Val Ser Gly Ile Lys
 85 90 95
 gga agt gga ggc tgg aca ctc act cgg cga ata gaa gac ctg tgg gaa 336
 Gly Ser Gly Gly Trp Thr Leu Thr Arg Arg Ile Glu Asp Leu Trp Glu
 100 105 110
 ctt cat ccg tcc ttt gac atc gtg gtc aac tgt tca ggc ctt gga agc 384
 Leu His Pro Ser Phe Asp Ile Val Val Asn Cys Ser Gly Leu Gly Ser
 115 120 125
 aga cag ctt gca gga gac tca aag att ttc cct gta agg ggc caa gtc 432
 Arg Gln Leu Ala Gly Asp Ser Lys Ile Phe Pro Val Arg Gly Gln Val
 130 135 140
 ctc caa gtt cag gct ccc tgg gtg gag cat ttt atc cga gat ggc agt 480
 Leu Gln Val Gln Ala Pro Trp Val Glu His Phe Ile Arg Asp Gly Ser
 145 150 155 160
 ggg ctg aca tat att tat cct ggt aca tcc cat gta acc cta ggt gga 528
 Gly Leu Thr Tyr Ile Tyr Pro Gly Thr Ser His Val Thr Leu Gly Gly
 165 170 175
 act agg caa aaa ggg gac tgg aat ctg tcc ccg gat gca gaa aat agc 576
 Thr Arg Gln Lys Gly Asp Trp Asn Leu Ser Pro Asp Ala Glu Asn Ser
 180 185 190
 aga gag att ctt tcc cga tgc tgt gct ctg gag ccc tcc ctc cac gga 624
 Arg Glu Ile Leu Ser Arg Cys Cys Ala Leu Glu Pro Ser Leu His Gly
 195 200 205
 gcc tgc aac atc agg gag aag gtg ggc ttg agg ccc tac agg cca ggc 672
 Ala Cys Asn Ile Arg Glu Lys Val Gly Leu Arg Pro Tyr Arg Pro Gly
 210 215 220
 gtg cga ctg cag aca gag ctc ctt gcg cga gat gga cag agg ctg cct 720
 Val Arg Leu Gln Thr Glu Leu Leu Ala Arg Asp Gly Gln Arg Leu Pro
 225 230 235 240

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gta gtc cac cac tat ggc cat ggg agt ggg ggc atc tca gtg cac tgg      768
Val Val His His Tyr Gly His Gly Ser Gly Gly Ile Ser Val His Trp
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ggc act gct ctg gag gcc gcc agg ctg gtg agc gag tgt gtc cat gcc      816
Gly Thr Ala Leu Glu Ala Ala Arg Leu Val Ser Glu Cys Val His Ala
                260                265                270
ctc agg acc ccc att ccc aag tca aac ctg tagatgacat aaaatgacag      866
Leu Arg Thr Pro Ile Pro Lys Ser Asn Leu
                275                280
caaagagact gagagactgt tgatcaaagc acagaacagg ttcaaataac ttttccactg      926
catgaaagtt taattagaca tttctttgtt ttcaacatta gaagtgggtgt aacatgtaag      986
ctgagcacgg tagcatgcct atagtccag ctacttg                                1023

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«210» 21
 «211» 341
 «212» PRT
 «213» Homo sapiens

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«400» 21
Met Asp Thr Ala Arg Ile Ala Val Val Gly Ala Gly Val Val Gly Leu
1                5                10                15
Ser Thr Ala Val Cys Ile Ser Lys Leu Val Pro Arg Cys Ser Val Thr
                20                25                30
Ile Ile Ser Asp Lys Phe Thr Pro Asp Thr Thr Ser Asp Val Ala Ala
                35                40                45
Gly Met Leu Ile Pro His Thr Tyr Pro Asp Thr Pro Ile His Thr Gln
                50                55                60
Lys Gln Trp Phe Arg Glu Thr Phe Asn His Leu Phe Ala Ile Ala Asn
65                70                75                80
Ser Ala Glu Ala Gly Asp Ala Gly Val His Leu Val Ser Gly Trp Gln
                85                90                95
Ile Phe Gln Ser Thr Pro Thr Glu Glu Val Pro Phe Trp Ala Asp Val
                100                105                110
Val Leu Gly Phe Arg Lys Met Thr Glu Ala Glu Leu Lys Lys Phe Pro
                115                120                125
Gln Tyr Val Phe Gly Gln Ala Phe Thr Thr Leu Lys Cys Glu Cys Pro
                130                135                140
Ala Tyr Leu Pro Trp Leu Glu Lys Arg Ile Lys Gly Ser Gly Gly Trp
145                150                155                160
Thr Leu Thr Arg Arg Ile Glu Asp Leu Trp Glu Leu His Pro Ser Phe
                165                170                175
Asp Ile Val Val Asn Cys Ser Gly Leu Gly Ser Arg Gln Leu Ala Gly
                180                185                190
Asp Ser Lys Ile Phe Pro Val Arg Gly Gln Val Leu Gln Val Gln Ala
                195                200                205
Pro Trp Val Glu His Phe Ile Arg Asp Gly Ser Gly Leu Thr Tyr Ile
                210                215                220
Tyr Pro Gly Thr Ser His Val Thr Leu Gly Gly Thr Arg Gln Lys Gly
225                230                235                240
Asp Trp Asn Leu Ser Pro Asp Ala Glu Asn Ser Arg Glu Ile Leu Ser
                245                250                255
Arg Cys Cys Ala Leu Glu Pro Ser Leu His Gly Ala Cys Asn Ile Arg
                260                265                270
Glu Lys Val Gly Leu Arg Pro Tyr Arg Pro Gly Val Arg Leu Gln Thr
                275                280                285
Glu Leu Leu Ala Arg Asp Gly Gln Arg Leu Pro Val Val His His Tyr
                290                295                300

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Gly His Gly Ser Gly Gly Ile Ser Val His Trp Gly Thr Ala Leu Glu
 305 310 315 320
 Ala Ala Arg Leu Val Ser Glu Cys Val His Ala Leu Arg Thr Pro Ile
 325 330 335
 Pro Lys Ser Asn Leu
 340

<210> 22
 <211> 282
 <212> PRT
 <213> Homo sapiens

<400> 22
 Met Asp Thr Ala Arg Ile Ala Val Val Gly Ala Gly Val Val Gly Leu
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 Ser Thr Ala Val Cys Ile Ser Lys Leu Val Pro Arg Cys Ser Val Thr
 20 25 30
 Ile Ile Ser Asp Lys Phe Thr Pro Asp Thr Thr Ser Asp Val Ala Ala
 35 40 45
 Gly Met Leu Ile Pro His Thr Tyr Pro Asp Thr Pro Ile His Thr Gln
 50 55 60
 Lys Gln Trp Phe Arg Glu Thr Phe Asn His Leu Phe Ala Ile Ala Asn
 65 70 75 80
 Ser Ala Glu Ala Gly Asp Ala Gly Val His Leu Val Ser Gly Ile Lys
 85 90 95
 Gly Ser Gly Gly Trp Thr Leu Thr Arg Arg Ile Glu Asp Leu Trp Glu
 100 105 110
 Leu His Pro Ser Phe Asp Ile Val Val Asn Cys Ser Gly Leu Gly Ser
 115 120 125
 Arg Gln Leu Ala Gly Asp Ser Lys Ile Phe Pro Val Arg Gly Gln Val
 130 135 140
 Leu Gln Val Gln Ala Pro Trp Val Glu His Phe Ile Arg Asp Gly Ser
 145 150 155 160
 Gly Leu Thr Tyr Ile Tyr Pro Gly Thr Ser His Val Thr Leu Gly Gly
 165 170 175
 Thr Arg Gln Lys Gly Asp Trp Asn Leu Ser Pro Asp Ala Glu Asn Ser
 180 185 190
 Arg Glu Ile Leu Ser Arg Cys Cys Ala Leu Glu Pro Ser Leu His Gly
 195 200 205
 Ala Cys Asn Ile Arg Glu Lys Val Gly Leu Arg Pro Tyr Arg Pro Gly
 210 215 220
 Val Arg Leu Gln Thr Glu Leu Leu Ala Arg Asp Gly Gln Arg Leu Pro
 225 230 235 240
 Val Val His His Tyr Gly His Gly Ser Gly Gly Ile Ser Val His Trp
 245 250 255
 Gly Thr Ala Leu Glu Ala Ala Arg Leu Val Ser Glu Cys Val His Ala
 260 265 270
 Leu Arg Thr Pro Ile Pro Lys Ser Asn Leu
 275 280

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<221> allele

<222> 24

<223> polymorphic base C or T

<400> 23

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47

<210> 24

<211> 47

<212> DNA

<213> Artificial Sequence

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<223> oligonucleotide 24-1457-52

<220>

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<222> 24

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<400> 24

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47

<210> 25

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 27-93-181

<220>

<221> allele

<222> 24

<223> polymorphic base C or T

<400> 25

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47

<210> 26

<211> 47

<212> DNA

<213> Artificial Sequence

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<223> oligonucleotide 24-1461-256

<220>

<221> allele

<222> 24

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<400> 26

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47